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# SEQUENCE LISTING

<110> Hageman, Gregory S.  
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<120> DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES

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<141> 2001-11-08

<150> US 09/430,195

<151> 1999-10-29

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<170> PatentIn Ver. 2.1

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<210> 6

<211> 198

<212> PRT

<213> Homo sapiens

<220>

<223> Human IPM 150 amino acid sequence, isoform C

<400> 6

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  1                               5           10          15

Gln Val Gln Gly Thr Lys Asp Ile Ser Ile Asn Ile Tyr His Ser Glu
                20                   25           30

Thr Lys Asp Ile Asp Asn Pro Pro Arg Asn Glu Thr Thr Glu Ser Thr
  35                   40                   45

Glu Lys Met Tyr Lys Met Ser Thr Met Arg Arg Ile Phe Asp Leu Ala
  50                   55                   60

Lys His Arg Thr Lys Arg Ser Ala Phe Phe Pro Thr Gly Val Lys Val
  65                   70                   75                   80

Cys Pro Gln Glu Ser Ser Met Lys Gln Ile Leu Asp Ser Leu Gln Ala Tyr
                85                   90                   95

Tyr Arg Leu Arg Val Cys Gln Glu Ala Ala Trp Glu Ala Tyr Arg Ile
  100                   105                   110

Phe Leu Asp Arg Ile Pro Asp Thr Gly Glu Tyr Gln Asp Trp Val Ser
  115                   120                   125

Ile Cys Gln Gln Glu Thr Phe Cys Leu Phe Asp Ile Gly Lys Asn Phe
  130                   135                   140

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Ser Asn Ser Gln Glu His Leu Asp Leu Leu Gln Gln Arg Ile Lys Gln  
145 150 155 160

Arg Ser Phe Pro Asp Arg Lys Asp Glu Ile Ser Ala Glu Lys Thr Leu  
165 170 175

Gly Glu Pro Gly Glu Thr Ile Val Ile Ser Thr Ala Ile Tyr Ile Ser  
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Lys Thr Trp Ala Val Phe  
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<210> 7

<211> 1858

<212> DNA

<213> Homo sapiens

<220>

<223> Human IMPG1 gene, regulatory region

<220>

<221> misc\_feature

<222> (1)..(1858)

<223> n i s a, c, g, o r t.

<400> 7

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<210> 8

<211> 3668  
 <212> DNA  
 <213> Mus sp.

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 <223> Mouse IPM 150 cDNA sequence, isoform A

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 <222> (1)..(3668)  
 <223> n is a, c, g, or t.

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<210> 9

<211> 798

<212> PRT

<213> Mus sp.

<220>

<223> Mouse IPM 150 amino acid sequence, isoform A

<400> 9

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Gln Val Gln Gly Ile Lys Asp Thr Ser Ile Lys Ile Phe Ser Ser Glu
                      20                      25                     30

```

```

Ile Lys Asn Ile Asp Lys Thr Pro Arg Ile Glu Thr Ile Glu Ser Thr
  35                      40                      45

```

```

Ser Thr Val His Lys Val Ser Thr Met Lys Arg Ile Phe Asp Leu Pro
  50                      55                      60

```

```

Lys Leu Arg Thr Lys Arg Ser Ala Leu Phe Pro Ala Ala Asn Ile Cys
  65                      70                      75                     80

```

```

Pro Gln Glu Ser Leu Arg Gln Ile Leu Ala Ser Leu Gln Glu Tyr Tyr
  85                      90                      95

```

```

Arg Leu Arg Val Cys Gln Glu Val Val Trp Glu Ala Tyr Arg Ile Phe
  100                     105                     110

```

```

Leu Asp Arg Ile Pro Asp Thr Glu Glu Tyr Gln Asp Trp Val Ser Leu
  115                     120                     125

```

```

Cys Gln Lys Glu Thr Phe Cys Leu Phe Asp Ile Gly Lys Asn Phe Ser
  130                     135                     140

```

```

Asn Ser Gln Glu His Leu Asp Leu Leu Gln Gln Arg Ile Lys Gln Arg
  145                     150                     155                     160

```

```

Ser Phe Pro Gly Arg Lys Asp Glu Thr Ala Ser Met Glu Thr Leu Glu
  165                     170                     175

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Ala Pro Thr Glu Ala Pro Val Val Pro Thr Asp Val Ser Arg Met Ser
  180                     185                     190

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Leu Gly Pro Phe Pro Leu Pro Ser Asp Asp Thr Asp Leu Lys Glu Ile  
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 Leu Ser Val Thr Leu Lys Asp Ile Gln Lys Pro Thr Thr Glu Ser Lys  
 210 215 220  
 Thr Glu Pro Ile His Val Ser Glu Phe Ser Ser Glu Glu Lys Val Glu  
 225 230 235 240  
 Phe Ser Ile Ser Leu Pro Asn His Arg Phe Lys Ala Glu Leu Thr Asn  
 245 250 255  
 Ser Gly Ser Pro Tyr Tyr Gln Glu Leu Val Gly Gln Ser Gln Leu Gln  
 260 265 270  
 Leu Gln Lys Ile Phe Lys Lys Leu Pro Gly Phe Gly Glu Ile Arg Val  
 275 280 285  
 Leu Gly Phe Arg Pro Lys Lys Glu Glu Asp Gly Ser Ser Ser Thr Glu  
 290 295 300  
 Ile Gln Leu Met Ala Ile Phe Lys Arg Asp His Ala Glu Ala Lys Ser  
 305 310 315 320  
 Pro Asp Ser His Leu Leu Ser Leu Asp Ser Asn Lys Ile Glu Ser Glu  
 325 330 335  
 Arg Ile His His Gly Val Ile Glu Asp Lys Gln Pro Glu Thr Tyr Leu  
 340 345 350  
 Thr Ala Thr Asp Leu Lys Lys Leu Ile Ile Gln Leu Leu Asp Gly Asp  
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 Leu Ser Leu Val Glu Gly Lys Ile Pro Phe Gly Asp Glu Val Thr Gly  
 370 375 380  
 Thr Leu Phe Arg Pro Val Thr Glu Pro Asp Leu Pro Lys Pro Leu Ala  
 385 390 395 400  
 Asp Val Thr Glu Asp Ala Thr Leu Ser Pro Glu Leu Pro Phe Val Glu  
 405 410 415  
 Pro Arg Leu Glu Ala Val Asp Arg Glu Gly Ser Glu Leu Pro Gly Met  
 420 425 430  
 Ser Ser Lys Asp Ser Ser Trp Ser Pro Pro Val Ser Ala Ser Ile Ser  
 435 440 445  
 Arg Ser Glu Asn Leu Pro Ser Phe Thr Pro Ser Ile Phe Ser Leu Asp  
 450 455 460  
 Ala Gln Ser Pro Pro Pro Leu Met Thr Thr Gly Pro Thr Ala Leu Ile  
 465 470 475 480  
 Pro Lys Pro Thr Leu Pro Thr Ile Asp Tyr Ser Thr Ile Arg Gln Leu  
 485 490 495  
 Pro Leu Glu Ser Ser His Trp Pro Ala Ser Ser Ser Asp Arg Glu Leu  
 500 505 510

Ile Thr Ser Ser His Asp Thr Ile Arg Asp Leu Asp Gly Met Asp Val  
 515 520 525  
 Ser Asp Thr Pro Ala Leu Ser Glu Ile Ser Glu Leu Ser Gly Tyr Asp  
 530 535 540  
 Ser Ala Ser Gly Gln Phe Leu Glu Met Thr Thr Pro Ile Pro Thr Val  
 545 550 555 560  
 Arg Phe Ile Thr Thr Ser Ser Glu Thr Ile Ala Thr Lys Gly Gln Glu  
 565 570 575  
 Leu Val Val Phe Phe Ser Leu Arg Val Ala Asn Met Pro Phe Ser Tyr  
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 Asp Leu Phe Asn Lys Ser Ser Leu Glu Tyr Gln Ala Leu Glu Gln Arg  
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 625 630 635 640  
 Ser Lys Val Arg Phe Ala Lys Ala Val Pro Tyr Asn Leu Thr Gln Ala  
 645 650 655  
 Val Arg Gly Val Leu Glu Asp Leu Arg Ser Thr Ala Ala Gln Gly Leu  
 660 665 670  
 Asn Leu Glu Ile Glu Ser Tyr Ser Leu Asp Ile Glu Pro Ala Asp Gln  
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 Ala Asp Pro Cys Lys Leu Leu Asp Cys Gly Lys Phe Ala Gln Cys Val  
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 Lys Asn Glu Trp Thr Glu Glu Ala Glu Cys Arg Cys Arg Gln Gly His  
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 Glu Ser His Gly Thr Leu Asp Tyr Gln Thr Leu Asn Leu Cys Pro Pro  
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 Gly Lys Thr Cys Val Ala Gly Arg Glu Gln Ala Thr Pro Cys Arg Pro  
 740 745 750  
 Pro Asp His Ser Thr Asn Gln Ala Gln Glu Pro Gly Val Lys Lys Leu  
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 Arg Gln Gln Asn Lys Val Val Lys Lys Arg Asn Ser Lys Leu Ser Ala  
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<210> 10  
 <211> 1726  
 <212> DNA  
 <213> Mus sp.

<220>

<223> Mouse IPM 150 cDNA sequence, isoform D

<400> 10

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<210> 11

<211> 466

<212> PRT

<213> Mus sp.

<220>

<223> Mouse IPM 150 amino acid sequence, isoform D

<400> 11

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Arg Ile Phe Leu Asp Arg Ile Pro Asp Thr Glu Glu Tyr Gln Asp Trp
          35            40            45
Val Ser Leu Cys Gln Lys Glu Thr Phe Cys Leu Phe Asp Ile Gly Lys
          50            55            60
Asn Phe Ser Asn Ser Gln Glu His Leu Asp Leu Leu Gln Gln Arg Ile
          65            70            75            80
Lys Gln Arg Ser Phe Pro Gly Arg Lys Asp Glu Thr Ala Ser Met Glu
          85            90            95

```

Thr Leu Glu Ala Pro Thr Glu Ala Pro Val Val Pro Thr Asp Val Ser  
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 Arg Met Ser Leu Gly Pro Phe Pro Leu Pro Ser Asp Asp Thr Asp Leu  
 115 120 125  
 Lys Glu Ile Leu Ser Val Thr Leu Lys Asp Ile Gln Lys Pro Thr Thr  
 130 135 140  
 Glu Ser Ile Thr Glu Pro Ile His Val Ser Glu Phe Ser Ser Glu Glu  
 145 150 155 160  
 Lys Val Glu Phe Ser Ile Ser Leu Pro Asn His Arg Phe Lys Ala Glu  
 165 170 175  
 Leu Thr Asn Ser Gly Ser Pro Tyr Tyr Gln Glu Leu Val Gly Gln Ser  
 180 185 190  
 Gln Leu Gln Leu Gln Lys Ile Phe Lys Lys Leu Pro Gly Phe Gly Glu  
 195 200 205  
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 210 215 220  
 Ser Thr Glu Ile Gln Leu Met Ala Ile Phe Lys Arg Asp His Ala Glu  
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 245 250 255  
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 260 265 270  
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 305 310 315 320  
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 340 345 350  
 Pro Ala Asp Gln Ala Asp Pro Cys Lys Leu Leu Asp Cys Gly Lys Phe  
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 Ala Gln Cys Val Lys Asn Glu Trp Thr Glu Glu Ala Glu Cys Arg Cys  
 370 375 380  
 Arg Gln Gly His Glu Ser His Gly Thr Leu Asp Tyr Gln Thr Leu Asn  
 385 390 395 400  
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 405 410 415



Pro Cys Arg Pro Thr Asp His Ser Thr Asn Gln Ala Gln Glu Pro Gly  
 420 425 430

Val Lys Lys Leu Arg Gln Gln Asn Lys Val Val Lys Lys Arg Asn Ser  
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Gly Asn  
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<210> 12  
 <211> 1321  
 <212> DNA  
 <213> Mus sp.

<220>  
 <223> Mouse IPM 150 cDNA sequence, isoform E

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 caccaccagc tccgagacca ttgccaccaa gggccaggag ctagtgggat tcttcagcct 480  
 gcgtgttggt aacatgccgt tctcctatga cctgttcaac aagagttctc tggagtatca 540  
 agccctggaa caacgattca cagacctgct ggttccctat cwacgatcga atcttacggg 600  
 atttaagcaa ctggaataac tcagcttcag aaacggaagt gtgatcgtga acagcaaaagt 660  
 gcggtttgca aaggcggtac cctacaacct caccaggcc gtgcgcgggg tcttggagga 720  
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 tgtaagaagt gagtggacag aggaagcaga gtgtcgctgc agacagggac atgagagcca 900  
 cgggaccctg gactaccaga ccctgaacct ctgtcccccct ggaagactt gtgtggcccg 960  
 ccgagaacaa gcaactccat gcaggccacc agatcactct acaaaaccaag ctccaggaacc 1020  
 tgggtgttaa aagctacgtc agcaaaataa ggtagtcaag aaacgaaatt ctaaactatc 1080  
 agctatagga ttgaaaaaat ttgaagacca ggactgggag ggaattataa agctggaatc 1140  
 atatgcatta ttgtgcaaac tctgttgaaa ggaacttta ttctttaaag aaaggtgtat 1200  
 ctgttctgtt aacttctgaa aaacagaggg agagattcag tggtcattgg aatacaggca 1260  
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 c 1321

<210> 13  
 <211> 67  
 <212> PRT  
 <213> Mus sp.

<220>  
 <223> Mouse IPM 150 amino acid sequence, isoform E

<400> 13  
 Met Asn Phe Gln Ile Lys His Ala Ile Phe Val Phe Gly Ile Phe Leu  
 1 5 10 15  
 Gln Val Gln Gly Ile Lys Asp Thr Ser Ile Lys Ile Phe Ser Ser Glu  
 20 25 30

Ile Lys Asn Ile Asp Lys Thr Pro Arg Ile Glu Thr Ile Glu Ser Thr  
35 40 45

Ser Thr Val His Lys Val Ser Thr Met Lys Arg Gln Pro Cys Gln Lys  
50 55 60

Tyr Gln Asn  
65

<210> 14

<211> 555

<212> DNA

<213> Unknown Organism

<220>

<223> Monkey IPM 150 cDNA (partial)

<220>

<223> Description of Unknown Organism: Monkey species

<400> 14

atcttctttc cgaacggggt taaagtctgt ccacaggaat ccatgaaca gattttagcc 60  
agtcttcaag cttattatag attgagagtg tgtcaggaag cagtatggga agcatatcgg 120  
atcttcttgg atcgcatccc tgacacaggg gaatatcagg actgggtcag cttctgccag 180  
caggagacct tctgcctctt tgacatcgga caaaacttca gcaattccca ggagcacctg 240  
gatcttctcc agcagagaat aaaacagaga agtttccttg agagaaaaga tgaagtatct 300  
acagagaaga cattgggaga gcctagtga accattgtgg ttccaacaga tgttgccagc 360  
gtctcaactg ggcttttccc tgtcactcct gatgacccc tcctcaatga aattctcgat 420  
aatgcactca acgacaccaa gatgcctaca acagaaagag aaacagaact cgctgtgtct 480  
gaggagcaga ggggtggagct cagcatctct ctgataaacc agaggttcaa ggagagctc 540  
gctgactctc agtca 555

<210> 15

<211> 185

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Monkey species

<220>

<223> Monkey IPM 150 amino acid sequence (partial).

<400> 15

Ile Phe Phe Pro Asn Gly Val Lys Val Cys Pro Gln Glu Ser Met Lys  
1 5 10 15

Gln Ile Leu Ala Ser Leu Gln Ala Tyr Tyr Arg Leu Arg Val Cys Gln  
20 25 30

Glu Ala Val Trp Glu Ala Tyr Arg Ile Phe Leu Asp Arg Ile Pro Asp  
35 40 45

Thr Gly Glu Tyr Gln Asp Trp Val Ser Phe Cys Gln Gln Glu Thr Phe  
50 55 60

Cys Leu Phe Asp Ile Gly Gln Asn Phe Ser Asn Ser Gln Glu His Leu  
65 70 75 80



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cttcaccata	tctgacctct	tctatacctt	ttggcttgga	ctccttgacc	tccaaagtca	1920
aagaccaatt	aaaagtgcgc	cttttctctg	cagatgcac	catggaaaaa	gagttaatat	1980
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aagtggaa	ggtttaacca	aaactcctgt	tctgaaactg	attagaagcc	tggagaagat	3960
ggagattact	tgttacttat	gtcatataat	taacctggat	tttaaacct	gttggagaag	4020
gagttttcta	tgaaaaaatt	aaatataggg	cacactgttt	tttttccagc	ttagttttc	4080
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taaatgtgaa	actacgtaaa	aaaaaa				4166

<210> 17  
 <211> 1241  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> Human IPM 200 amino acid sequence, isoform A

<400> 17  
 Met Ile Met Phe Pro Leu Phe Gly Lys Ile Ser Leu Gly Ile Leu Ile  
 1 5 10 15  
 Phe Val Leu Ile Glu Gly Asp Phe Pro Ser Leu Thr Ala Gln Thr Tyr  
 20 25 30  
 Leu Ser Ile Glu Glu Ile Gln Glu Pro Lys Ser Ala Val Ser Phe Leu  
 35 40 45

Leu Pro Glu Glu Ser Thr Asp Leu Ser Leu Ala Thr Lys Lys Lys Gln  
 50 55 60  
 Pro Leu Asp Arg Arg Glu Thr Glu Arg Gln Trp Leu Ile Arg Arg Arg  
 65 70 75 80  
 Arg Ser Ile Leu Phe Pro Asn Gly Val Lys Ile Cys Pro Asp Glu Ser  
 85 90 95  
 Val Ala Glu Ala Val Ala Asn His Val Lys Tyr Phe Lys Val Arg Val  
 100 105 110  
 Cys Gln Glu Ala Val Trp Glu Ala Phe Arg Thr Phe Trp Asp Arg Leu  
 115 120 125  
 Pro Gly Arg Glu Glu Tyr His Tyr Trp Met Asn Leu Cys Glu Asp Gly  
 130 135 140  
 Val Thr Ser Ile Phe Glu Met Gly Thr Asn Phe Ser Glu Ser Val Glu  
 145 150 155 160  
 His Arg Ser Leu Ile Met Lys Lys Leu Thr Tyr Ala Lys Glu Thr Val  
 165 170 175  
 Ser Ser Ser Glu Leu Ser Ser Pro Val Pro Val Gly Asp Thr Ser Thr  
 180 185 190  
 Leu Gly Asp Thr Thr Leu Ser Val Pro His Pro Glu Val Asp Ala Tyr  
 195 200 205  
 Glu Gly Ala Ser Glu Ser Ser Leu Glu Arg Pro Glu Glu Ser Ile Ser  
 210 215 220  
 Asn Glu Ile Glu Asn Val Ile Glu Glu Ala Thr Lys Pro Ala Gly Glu  
 225 230 235 240  
 Gln Ile Ala Glu Phe Ser Ile His Leu Leu Gly Lys Gln Tyr Arg Glu  
 245 250 255  
 Glu Leu Gln Asp Ser Ser Ser Phe His His Gln His Leu Glu Glu Glu  
 260 265 270  
 Phe Ile Ser Glu Val Glu Asn Ala Phe Thr Gly Leu Pro Gly Tyr Lys  
 275 280 285  
 Glu Ile Arg Val Leu Glu Phe Arg Ser Pro Lys Glu Asn Asp Ser Gly  
 290 295 300  
 Val Asp Val Tyr Tyr Ala Val Thr Phe Asn Gly Glu Ala Ile Ser Asn  
 305 310 315 320  
 Thr Thr Trp Asp Leu Ile Ser Leu His Ser Asn Lys Val Glu Asn His  
 325 330 335  
 Gly Leu Val Glu Leu Asp Asp Lys Pro Thr Val Val Tyr Thr Ile Ser  
 340 345 350  
 Asn Phe Arg Asp Tyr Ile Ala Glu Thr Leu Gln Gln Asn Phe Leu Leu  
 355 360 365

Gly Asn Ser Ser Leu Asn Pro Asp Pro Asp Ser Leu Gln Leu Ile Asn  
 370 375 380  
 Val Arg Gly Val Leu Arg His Gln Thr Glu Asp Leu Val Trp Asn Thr  
 385 390 395 400  
 Gln Ser Ser Ser Leu Gln Ala Thr Pro Ser Ser Ile Leu Asp Asn Thr  
 405 410 415  
 Phe Gln Ala Ala Trp Pro Ser Ala Asp Glu Ser Ile Thr Ser Ser Ile  
 420 425 430  
 Pro Pro Leu Asp Phe Ser Ser Gly Pro Pro Ser Ala Thr Gly Arg Glu  
 435 440 445  
 Leu Trp Ser Glu Ser Pro Leu Gly Asp Leu Val Ser Thr His Lys Leu  
 450 455 460  
 Ala Phe Pro Ser Lys Met Gly Leu Ser Ser Ser Pro Glu Val Leu Glu  
 465 470 475 480  
 Val Ser Ser Leu Thr Leu His Ser Val Thr Pro Ala Val Leu Gln Thr  
 485 490 495  
 Gly Leu Pro Val Ala Ser Glu Glu Arg Thr Ser Gly Ser His Leu Val  
 500 505 510  
 Glu Asp Gly Leu Ala Asn Val Glu Glu Ser Glu Asp Phe Leu Ser Ile  
 515 520 525  
 Asp Ser Leu Pro Ser Ser Ser Phe Thr Gln Pro Val Pro Lys Glu Thr  
 530 535 540  
 Ile Pro Ser Met Glu, Asp Ser Asp Val Ser Leu Thr Ser Ser Pro Tyr  
 545 550 555 560  
 Leu Thr Ser Ser Ile Pro Phe Gly Leu Asp Ser Leu Thr Ser Lys Val  
 565 570 575  
 Lys Asp Gln Leu Lys Val Ser Pro Phe Leu Pro Asp Ala Ser Met Glu  
 580 585 590  
 Lys Glu Leu Ile Phe Asp Gly Gly Leu Gly Ser Gly Ser Gly Gln Lys  
 595 600 605  
 Val Asp Leu Ile Thr Trp Pro Trp Ser Glu Thr Ser Ser Glu Lys Ser  
 610 615 620  
 Ala Glu Pro Leu Ser Lys Pro Trp Leu Glu Asp Asp Asp Ser Leu Leu  
 625 630 635 640  
 Pro Ala Glu Ile Glu Asp Lys Lys Leu Val Leu Val Asp Lys Met Asp  
 645 650 655  
 Ser Thr Asp Gln Ile Ser Lys His Ser Lys Tyr Glu His Asp Asp Arg  
 660 665 670  
 Ser Thr His Phe Pro Glu Glu Glu Pro Leu Ser Gly Pro Ala Val Pro  
 675 680 685

Ile Phe Ala Asp Thr Ala Ala Glu Ser Ala Ser Leu Thr Leu Pro Lys  
 690 695 700  
 His Ile Ser Glu Val Pro Gly Val Asp Asp Cys Ser Val Thr Lys Ala  
 705 710 715 720  
 Pro Leu Ile Leu Thr Ser Val Ala Ile Ser Ala Ser Thr Asp Lys Ser  
 725 730 735  
 Asp Gln Ala Asp Ala Ile Leu Arg Glu Asp Met Glu Gln Ile Thr Glu  
 740 745 750  
 Ser Ser Asn Tyr Glu Trp Phe Asp Ser Glu Val Ser Met Val Lys Pro  
 755 760 765  
 Asp Met Gln Thr Leu Trp Thr Ile Leu Pro Glu Ser Glu Arg Val Trp  
 770 775 780  
 Thr Arg Thr Ser Ser Leu Glu Lys Leu Ser Arg Asp Ile Leu Ala Ser  
 785 790 795 800  
 Thr Pro Gln Ser Ala Asp Arg Leu Trp Leu Ser Val Thr Gln Ser Thr  
 805 810 815  
 Lys Leu Pro Pro Thr Thr Ile Ser Thr Leu Leu Glu Asp Glu Val Ile  
 820 825 830  
 Met Gly Val Gln Asp Ile Ser Leu Glu Leu Asp Arg Ile Gly Thr Asp  
 835 840 845  
 Tyr Tyr Gln Pro Glu Gln Val Gln Glu Gln Asn Gly Lys Val Gly Ser  
 850 855 860  
 Tyr Val Glu Met Ser Thr Ser Val His Ser Thr Glu Met Val Ser Val  
 865 870 875 880  
 Ala Trp Pro Thr Glu Gly Gly Asp Asp Leu Ser Tyr Thr Gln Thr Ser  
 885 890 895  
 Gly Ala Leu Val Val Phe Phe Ser Leu Arg Val Thr Asn Met Met Phe  
 900 905 910  
 Ser Glu Asp Leu Phe Asn Lys Asn Ser Leu Glu Tyr Lys Ala Leu Glu  
 915 920 925  
 Gln Arg Phe Leu Glu Leu Leu Val Pro Tyr Leu Gln Ser Asn Leu Thr  
 930 935 940  
 Gly Phe Gln Asn Leu Glu Ile Leu Asn Phe Arg Asn Gly Ser Ile Val  
 945 950 955 960  
 Val Asn Ser Arg Met Lys Phe Ala Asn Ser Val Pro Pro Asn Val Asn  
 965 970 975  
 Asn Ala Val Tyr Met Ile Leu Glu Asp Phe Cys Thr Thr Ala Tyr Asn  
 980 985 990  
 Thr Met Asn Leu Ala Ile Asp Lys Tyr Ser Leu Asp Val Glu Ser Gly  
 995 1000 1005

Asp Glu Ala Asn Pro Cys Lys Phe Gln Ala Cys Asn Glu Phe Ser Glu  
 1010 1015 1020  
 Cys Leu Val Asn Pro Trp Ser Gly Glu Ala Lys Cys Arg Cys Phe Pro  
 1025 1030 1035 1040  
 Gly Tyr Leu Ser Val Glu Glu Arg Pro Cys Gln Ser Leu Cys Asp Leu  
 1045 1050 1055  
 Gln Pro Asp Phe Cys Leu Asn Asp Gly Lys Cys Asp Ile Met Pro Gly  
 1060 1065 1070  
 His Gly Ala Ile Cys Arg Cys Arg Val Gly Glu Asn Trp Trp Tyr Arg  
 1075 1080 1085  
 Gly Lys His Cys Glu Glu Phe Val Ser Glu Pro Val Ile Ile Gly Ile  
 1090 1095 1100  
 Thr Ile Ala Ser Val Val Gly Leu Leu Val Ile Phe Ser Ala Ile Ile  
 1105 1110 1115 1120  
 Tyr Phe Phe Ile Arg Thr Leu Gln Ala His His Asp Arg Ser Glu Arg  
 1125 1130 1135  
 Glu Ser Pro Phe Ser Gly Ser Ser Arg Gln Pro Asp Ser Leu Ser Ser  
 1140 1145 1150  
 Ile Glu Asn Ala Val Lys Tyr Asn Pro Val Tyr Glu Ser His Arg Ala  
 1155 1160 1165  
 Gly Cys Glu Lys Tyr Glu Gly Pro Tyr Pro Gln His Pro Phe Tyr Ser  
 1170 1175 1180  
 Ser Ala Ser Gly Asp Val Ile Gly Gly Leu Ser Arg Glu Glu Ile Arg  
 1185 1190 1195 1200  
 Gln Met Tyr Glu Ser Ser Glu Leu Ser Arg Glu Glu Ile Gln Glu Arg  
 1205 1210 1215  
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 1220 1225 1230  
 Val Arg Glu Gln Gln Val Glu Glu Val  
 1235 1240

<210> 18

<211> 2964

<212> DNA

<213> Homo sapiens

<220>

<223> Human IPM 200 cDNA sequence, isoform C

<400> 18

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 ctctgggtat ttgatatttt gtccgtgatag aaggagactt tccatcatta acagcacaaa 180  
 cctactttatc tatagaggag atccaagaac ccaagagtgc agtttctttt ctctgtcctg 240  
 aagaatcaac agacctttct ctagtacca aaaagaaaca gcctctggac cgcagagaaa 300  
 ctgaagaca gtggttaatc agaaggcgga gatctattct gtttctctaat ggagtgaaaa 360



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<210> 19

<211> 432

<212> PRT

<213> Homo sapiens

<220>

<223> Human IPM 200 amino acid sequence, isoform C

<220>

<221> UNSURE

<222> (1)..(432)

<223> Xaa is any amino acid.

<400> 19

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 Phe Val Leu Ile Glu Gly Asp Phe Pro Ser Leu Thr Ala Gln Thr Tyr  
 20 25 30  
 Leu Ser Ile Glu Glu Ile Gln Glu Pro Lys Ser Ala Val Ser Phe Leu  
 35 40 45  
 Leu Pro Glu Glu Ser Thr Asp Leu Ser Leu Ala Thr Lys Lys Lys Gln  
 50 55 60  
 Pro Leu Asp Arg Arg Glu Thr Glu Arg Gln Trp Leu Ile Arg Arg Arg  
 65 70 75 80  
 Arg Ser Ile Leu Phe Pro Asn Gly Val Lys Ile Cys Pro Asp Glu Ser  
 85 90 95  
 Val Ala Glu Ala Val Ala Asn His Val Lys Tyr Phe Lys Val Arg Val  
 100 105 110  
 Cys Gln Glu Ala Val Trp Glu Ala Phe Arg Thr Phe Trp Asp Xaa Leu  
 115 120 125  
 Pro Gly Arg Glu Glu Tyr His Tyr Trp Met Asn Leu Cys Glu Asp Gly  
 130 135 140  
 Val Thr Ser Ile Phe Glu Met Gly Thr Asn Phe Ser Glu Ser Val Glu  
 145 150 155 160  
 His Arg Ser Leu Ile Met Lys Lys Leu Thr Tyr Ala Lys Glu Thr Val  
 165 170 175  
 Ser Ser Ser Glu Leu Ser Ser Pro Val Pro Val Gly Asp Thr Ser Thr  
 180 185 190  
 Leu Gly Asp Thr Thr Leu Ser Val Pro His Pro Glu Val Asp Ala Tyr  
 195 200 205  
 Glu Gly Ala Ser Glu Ser Ser Leu Glu Arg Pro Glu Glu Ser Ile Ser  
 210 215 220  
 Asn Glu Ile Glu Asn Val Ile Glu Glu Ala Thr Lys Pro Ala Gly Glu  
 225 230 235 240  
 Gln Ile Ala Glu Phe Ser Ile His Leu Leu Gly Lys Gln Tyr Arg Glu  
 245 250 255  
 Glu Leu Gln Asp Ser Ser Ser Phe His His Gln His Leu Glu Glu Glu  
 260 265 270  
 Phe Ile Ser Glu Val Glu Asn Ala Phe Thr Gly Leu Pro Gly Tyr Lys  
 275 280 285  
 Glu Ile Arg Val Leu Glu Phe Arg Ser Pro Lys Glu Asn Asp Ser Gly  
 290 295 300  
 Val Asp Val Tyr Tyr Ala Val Thr Phe Asn Gly Glu Ala Ile Ser Asn  
 305 310 315 320

Thr Thr Trp Asp Leu Ile Ser Leu His Ser Asn Lys Val Glu Asn His  
 325 330 335  
 Gly Leu Val Glu Leu Asp Asp Lys Pro Thr Val Val Tyr Thr Ile Ser  
 340 345 350  
 Asn Phe Arg Asp Tyr Ile Ala Glu Thr Leu Gln Gln Asn Phe Leu Leu  
 355 360 365  
 Gly Asn Ser Ser Leu Asn Pro Asp Pro Asp Ser Leu Gln Leu Ile Asn  
 370 375 380  
 Val Arg Gly Val Leu Arg His Gln Thr Glu Asp Leu Val Trp Asn Thr  
 385 390 395 400  
 Gln Ser Ser Ser Leu Gln Ala Thr Pro Ser Ser Ile Leu Cys Phe Xaa  
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 <211> 861  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> Human IPM 200 cDNA sequence, isoform F

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 ttgtcctgat agaaggagac ttcccatcat taacagcaca aacctactta tctatagagg 180  
 agatccaagc actgtgagga atttgtgtct gagcccgatg tcataggcat cactattgcc 240  
 tccgtggttg gactcttgtt catcttttct gctatcatct acttcttcat caggactctt 300  
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 acctggattt taaacactgt tggaagaaga gttttctatg aaaaaattaa atatagggca 780  
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 tctataaaga ctgaatgctg t 861

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 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> Human IPM 200 amino acid sequence, isoform F

<400> 21

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Phe Val Leu Ile Glu Gly Asp Phe Pro Ser Leu Thr Ala Gln Thr Tyr  
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Leu Ser Ile Glu Glu Ile Gln Ala Leu  
 35 40

<210> 22  
 <211> 3011  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> Human IPM 200, regulatory region

<220>  
 <221> misc\_feature  
 <222> (1)..(3011)  
 <223> n i a a, c, g, or t.

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 aaaatcaaat attaagtgat aaaaccaaga tttagagcca ggggttctca atcttaataa 240  
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<210> 23

<211> 4204

<212> DNA

<213> Mus sp.

<220>

<223> Mouse IPM 200 cDNA sequence (partial)

<220>

<221> misc\_feature

<222> (1)..(4204)

<223> n is a, c, g, or t.

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aacatagaaa	cctaactcat	aagaaaactgg	cttacacaag	ggaagctgag	agcagctcct	240
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ggaa 4204

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<210> 24
<211> 1069
<212> PRT
<213> Mus sp.

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<220>
<223> Mouse IPM 200 amino acid sequence (partial)

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<220>
<221> UNSURE
<222> (1)..(1069)
<223> Xaa is any amino acid.

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Ile Trp Glu Ala Phe Arg Thr Phe Trp Asp Arg Leu Pro Gly Arg Asp
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Glu Tyr Arg His Trp Met Asn Leu Cys Glu Asp Gly Val Thr Ser Val  
 35 40 45  
 Phe Glu Met Gly Ala His Phe Ser Gln Ser Val Glu His Arg Asn Leu  
 50 55 60  
 Ile Met Lys Lys Leu Ala Tyr Thr Arg Glu Ala Glu Ser Ser Ser Cys  
 65 70 75 80  
 Lys Asp Gln Ser Cys Gly Pro Glu Leu Ser Phe Pro Val Pro Ile Gly  
 85 90 95  
 Glu Thr Ser Thr Leu Thr Gly Ala Val Ser Ser Ala Ser Tyr Pro Gly  
 100 105 110  
 Leu Ala Ser Glu Ser Ser Ala Ala Ser Pro Gln Glu Ser Ile Ser Asn  
 115 120 125  
 Glu Ile Glu Asn Val Thr Glu Glu Pro Thr Gln Pro Ala Ala Glu Gln  
 130 135 140  
 Ile Ala Glu Phe Ser Ile Gln Leu Leu Gly Lys Arg Tyr Ser Glu Glu  
 145 150 155 160  
 Leu Arg Asp Pro Ser Ser Ala Leu Tyr Arg Leu Leu Val Glu Glu Phe  
 165 170 175  
 Ile Ser Glu Val Glu Lys Ala Phe Thr Gly Leu Pro Gly Tyr Lys Gly  
 180 185 190  
 Ile Arg Val Leu Glu Phe Arg Ala Pro Glu Glu Asn Asp Ser Gly Ile  
 195 200 205  
 Asp Val His Tyr Ala Val Thr Phe Asn Gly Glu Ala Ile Ser Asn Thr  
 210 215 220  
 Thr Trp Asp Leu Ile Ser Leu His Ser Asn Lys Val Glu Asn His Gly  
 225 230 235 240  
 Leu Val Glu Met Asp Asp Lys Pro Thr Ala Val Tyr Thr Ile Ser Asn  
 245 250 255  
 Phe Arg Asp Tyr Ile Ala Glu Thr Leu His Gln Asn Phe Leu Met Gly  
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 275 280 285  
 Arg Gly Val Leu Leu Pro Gln Thr Glu Asp Ile Val Trp Asn Thr Gln  
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 Ser Ser Ser Leu Gln Val Thr Thr Ser Ser Ile Xaa Val Leu Gln Pro  
 305 310 315 320  
 Asp Leu Pro Val Ala Pro Glu Gly Arg Thr Ser Gly Ser Phe Ile Leu  
 325 330 335  
 Glu Asp Gly Leu Ala Ser Thr Glu Glu Leu Glu Asp Thr Ser Ile Asp  
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Gly Leu Pro Ser Ser Pro Leu Ile Gln Pro Val Pro Lys Glu Thr Val  
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 465 470 475 480  
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 660 665 670



Asp Gln Val Gly Thr Asp Tyr Tyr Gln Ser Glu Leu Thr Glu Glu Gln  
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His Gly Lys Ala Asp Ser Tyr Val Glu Met Ser Thr Ser Val His Tyr  
 690 695 700

Thr Glu Met Pro Ile Val Ala Leu Pro Thr Lys Gly Gly Val Leu Ser  
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His Thr Gln Thr Ala Gly Ala Leu Val Val Phe Phe Ser Leu Arg Val  
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Thr Asn Met Leu Phe Ser Glu Asp Leu Phe Asn Lys Asn Ser Leu Glu  
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Tyr Lys Ala Leu Glu Gln Arg Phe Leu Glu Leu Leu Ala Pro Tyr Leu  
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Gln Ser Asn Leu Ser Gly Phe Gln Asn Leu Glu Ile Leu Ser Phe Arg  
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Asn Gly Ser Ile Val Val Asn Ser Arg Val Arg Phe Ala Glu Ser Ala  
 785 790 795 800

Pro Pro Asn Val Asn Lys Ala Met Tyr Arg Ile Leu Glu Asp Phe Cys  
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Thr Thr Ala Tyr Gln Thr Met Asn Leu Asp Ile Asp Lys Tyr Ser Leu  
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Asp Val Glu Ser Gly Asp Glu Ala Asn Pro Cys Lys Phe Gln Ala Cys  
 835 840 845

Asn Glu Phe Ser Glu Cys Leu Val Asn Pro Trp Ser Gly Glu Ala Lys  
 850 855 860

Cys Lys Cys Tyr Pro Gly Tyr Leu Ser Val Asp Glu Leu Pro Cys Gln  
 865 870 875 880

Ser Leu Cys Asp Leu Gln Pro Asp Phe Cys Leu Asn Asp Gly Lys Cys  
 885 890 895

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 900 905 910

Asn Trp Trp Tyr Arg Gly Gln His Cys Glu Glu Phe Val Ser Glu Pro  
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Phe Val Ile Gly Ile Thr Ile Ala Ser Val Val Ser Phe Leu Leu Val  
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Ala Ser Ala Val Val Phe Phe Leu Val Lys Met Leu Gln Ala Gln Asn  
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Val Arg Arg Glu Arg Gln Arg Pro Thr Ser Ser Ser Arg His Pro Asp  
 965 970 975

Ser Leu Ser Ser Val Glu Asn Ala Met Lys Tyr Asn Pro Ala Tyr Glu  
 980 985 990

Ser His Leu Ala Gly Cys Glu Leu Tyr Glu Lys Ser Tyr Ser Gln His  
995 1000 1005

Pro Phe Tyr Ser Ser Ala Ser Glu Glu Val Ile Gly Gly Leu Ser Arg  
1010 1015 1020

Glu Glu Ile Arg Gln Met Tyr Glu Ser Ser Asp Leu Ser Lys Glu Glu  
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<211> 546

<212> DNA

<213> Macaca fascicularis

<220>

<223> Monkey IPM 200 cDNA sequence (partial)

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gcggagatct attctgtttc ctaatggagt aaaaatctgc ccagatgaaa gtgttacaga 480  
ggctgtggca aatcatgtga agtattttaa agtccgagtg tgtcaggaag ctgtctggga 540  
aaagcc 546

<210> 26

<211> 119

<212> PRT

<213> Macaca fascicularis

<220>

<223> Monkey IPM 200 amino acid sequence (partial)

<400> 26

Met Ile Met Phe Pro Leu Phe Gly Lys Ile Ser Leu Gly Ile Leu Ile  
1 5 10 15

Phe Val Leu Ile Gly Asp Phe Pro Ser Leu Thr Ala Gln Thr Tyr Leu  
20 25 30

Ser Leu Glu Glu Ile Gln Glu Pro Lys Ser Ala Val Ser Phe Leu Leu  
35 40 45

Pro Glu Glu Ser Thr Asp Leu Ser Leu Ala Thr Lys Lys Lys Gln Pro  
50 55 60

Leu Asp Leu Arg Glu Thr Glu Arg Gln Trp Leu Leu Arg Arg Arg Arg  
65 70 75 80

Ser Ile Leu Phe Pro Asn Gly Val Lys Ile Cys Pro Asp Glu Ser Val  
85 90 95

Thr Glu Ala Val Ala Asn His Val Lys Tyr Phe Lys Val Arg Val Cys  
100 105 110

Gln Glu Ala Val Trp Glu Lys  
115

<210> 27  
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<212> DNA  
<213> Homo sapiens

<220>  
<223> Human IPM 150 isoform A variant cDNA sequence

<220>  
<221> CDS  
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agccaga atg tat ttg gaa act aga aga gct att ttt gtt ttt tgg att 169  
Met Tyr Leu Glu Thr Arg Arg Ala Ile Phe Val Phe Trp Ile  
1 5 10

ttt ctc caa gtt caa gga act aaa gat atc tcc att aac ata tac cat 217  
Phe Leu Gln Val Gln Gly Thr Lys Asp Ile Ser Ile Asn Ile Tyr His  
15 20 25 30

tct gaa act aaa gac ata gac aat ccc cca aga aat gaa aca act gaa 265  
Ser Glu Thr Lys Asp Ile Asp Asn Pro Pro Arg Asn Glu Thr Thr Glu  
35 40 45

agt act gaa aaa atg tac aaa atg tca act atg aga cga ata ttc gat. 313  
Ser Thr Glu Lys Met Tyr Lys Met Ser Thr Met Arg Arg Ile Phe Asp  
50 55 60

ttg gca aag cat cga aca aaa aga tcc gca ttt ttc cca acg ggg gtt 361  
Leu Ala Lys His Arg Thr Lys Arg Ser Ala Phe Phe Pro Thr Gly Val  
65 70 75

aaa gtc tgt cca cag gaa tcc atg aaa cag att tta gac agt ctt caa 409  
Lys Val Cys Pro Gln Glu Ser Met Lys Gln Ile Leu Asp Ser Leu Gln  
80 85 90

gct tat tat aga ttg aga gtg tgt cag gaa gca gta tgg gaa gca tat 457  
Ala Tyr Tyr Arg Leu Arg Val Cys Gln Glu Ala Val Trp Glu Ala Tyr  
95 100 105 110

cgg atc ttt ctg gat cgc atc cct gac aca ggg gaa tat cag gac tgg 505  
Arg Ile Phe Leu Asp Arg Ile Pro Asp Thr Gly Glu Tyr Gln Asp Trp  
115 120 125

gtc agc atc tgc cag cag gag acc ttc tgc ctc ttt gac att gga aaa	553
Val Ser Ile Cys Gln Gln Glu Thr Phe Cys Leu Phe Asp Ile Gly Lys	
130 135 140	
aac ttc agc aat tcc cag gag cac ctg gat ctt ctc cag cag aga ata	601
Asn Phe Ser Asn Ser Gln Glu His Leu Asp Leu Leu Gln Gln Arg Ile	
145 150 155	
aaa cag aga agt ttc cct gac aga aaa gat gaa ata tct gca gag aag	649
Lys Gln Arg Ser Phe Pro Asp Arg Lys Asp Glu Ile Ser Ala Glu Lys	
160 165 170	
aca ttg gga gag cct ggt gaa acc att gtc att tca aca gat gtt gcc	697
Thr Leu Gly Glu Pro Gly Glu Thr Ile Val Ile Ser Thr Asp Val Ala	
175 180 185 190	
aac gtc tca ctt ggg cct ttc cct ctc act cct gat gac acc ctc ctc	745
Asn Val Ser Leu Gly Pro Phe Pro Leu Thr Pro Asp Asp Thr Leu Leu	
195 200 205	
aat gaa att ctc gat aat aca ctc aac gac acc aag atg cct aca aca	793
Asn Glu Ile Leu Asp Asn Thr Leu Asn Asp Thr Lys Met Pro Thr Thr	
210 215 220	
gaa aga gaa aca gaa ttc gct gtg ttg gag gag cag agg gtg gag ctc	841
Glu Arg Glu Thr Glu Phe Ala Val Leu Glu Glu Gln Arg Val Glu Leu	
225 230 235	
agc gtc tct ctg gta aac cag aag ttc aag gca gag ctc gct gac tcc	889
Ser Val Ser Leu Val Asn Gln Lys Phe Lys Ala Glu Leu Ala Asp Ser	
240 245 250	
cag tcc cca tat tac cag gag cta gca gga aag tcc caa ctt cag atg	937
Gln Ser Pro Tyr Tyr Gln Glu Leu Ala Gly Lys Ser Gln Leu Gln Met	
255 260 265 270	
caa aag ata ttt aag aaa ctt cca gga ttc aaa aaa atc cat gtg tta	985
Gln Lys Ile Phe Lys Lys Leu Pro Gly Phe Lys Lys Ile His Val Leu	
275 280 285	
gga ttt aga cca aag aaa gaa aaa gat ggc tca agc tcc aca gag atg	1033
Gly Phe Arg Pro Lys Lys Glu Lys Asp Gly Ser Ser Ser Thr Glu Met	
290 295 300	
caa ctt acg gcc atc ttt aag aga cac agt gca gaa gca aaa agc cct	1081
Gln Leu Thr Ala Ile Phe Lys Arg His Ser Ala Glu Ala Lys Ser Pro	
305 310 315	
gca agt gac ctc ctg tct ttt gat tcc aac aaa att gaa agt gag gaa	1129
Ala Ser Asp Leu Leu Ser Phe Asp Ser Asn Lys Ile Glu Ser Glu Glu	
320 325 330	
gtc tat cat gga acc atg gag gag gac aag caa cca gaa atc tat ctc	1177
Val Tyr His Gly Thr Met Glu Glu Asp Lys Gln Pro Glu Ile Tyr Leu	
335 340 345 350	
aca gct aca gac ctc aaa agg ctg atc agc aaa gca cta gag gaa gaa	1225
Thr Ala Thr Asp Leu Lys Arg Leu Ile Ser Lys Ala Leu Glu Glu Glu	
355 360 365	

caa tct ttg gat gtg ggg aca att cag ttc act gat gaa att gct gga	1273
Gln Ser Leu Asp Val Gly Thr Ile Gln Phe Thr Asp Glu Ile Ala Gly	
370 375 380	
tca ctg cca gcc ttt ggt cct gac acc caa tca gag ctg ccc aca tct	1321
Ser Leu Pro Ala Phe Gly Pro Asp Thr Gln Ser Glu Leu Pro Thr Ser	
385 390 395	
ttt gct gtt ata aca gag gat gct act ttg agt cca gaa ctt cct cct	1369
Phe Ala Val Ile Thr Glu Asp Ala Thr Leu Ser Pro Glu Leu Pro Pro	
400 405 410	
gtt gaa ccc cag ctt gag aca gtg gac gga gca gag cat ggt cta cct	1417
Val Glu Pro Gln Leu Glu Thr Val Asp Gly Ala Glu His Gly Leu Pro	
415 420 425 430	
gac act tct tgg tct cca cct gct atg gcc tct acc tcc ctg tca gaa	1465
Asp Thr Ser Trp Ser Pro Pro Ala Met Ala Ser Thr Ser Leu Ser Glu	
435 440 445	
gct cca cct ttc ttt atg gca tca agc atc ttc tct ctg act gat caa	1513
Ala Pro Pro Phe Phe Met Ala Ser Ser Ile Phe Ser Leu Thr Asp Gln	
450 455 460	
ggc acc aca gat aca atg gcc act gac cag aca atg cta gta cca ggg	1561
Gly Thr Thr Asp Thr Met Ala Thr Asp Gln Thr Met Leu Val Pro Gly	
465 470 475	
ctc acc atc ccc acc agt gat tat tct gca atc agc caa ctg gct ctg	1609
Leu Thr Ile Pro Thr Ser Asp Tyr Ser Ala Ile Ser Gln Leu Ala Leu	
480 485 490	
gga att tca cat cca cct gca tct tca gat gac agc cga tca agt gca	1657
Gly Ile Ser His Pro Pro Ala Ser Ser Asp Asp Ser Arg Ser Ser Ala	
495 500 505 510	
ggt ggc gaa gat atg gtc aga cac cta gat gaa atg gat ctg tct gac	1705
Gly Gly Glu Asp Met Val Arg His Leu Asp Glu Met Asp Leu Ser Asp	
515 520 525	
act cct gcc cca tct gag gta cca gag ctc agc gaa tat gtt tct gtc	1753
Thr Pro Ala Pro Ser Glu Val Pro Glu Leu Ser Glu Tyr Val Ser Val	
530 535 540	
cca gat cat ttc ttg gag gat acc act cct gtc tca gct tta cag tat	1801
Pro Asp His Phe Leu Glu Asp Thr Thr Pro Val Ser Ala Leu Gln Tyr	
545 550 555	
atc acc act agt tct atg acc att gcc ccc aag ggc cga gag ctg gta	1849
Ile Thr Thr Ser Ser Met Thr Ile Ala Pro Lys Gly Arg Glu Leu Val	
560 565 570	
gtg ttc ttc agt ctg cgt gtt gct aac atg gcc ttc tcc aac gac ctg	1897
Val Phe Phe Ser Leu Arg Val Ala Asn Met Ala Phe Ser Asn Asp Leu	
575 580 585 590	
ttc aac aag agc tct ctg gag tac cga gct ctg gag caa caa ttc aca	1945
Phe Asn Lys Ser Ser Leu Glu Tyr Arg Ala Leu Glu Gln Gln Phe Thr	
595 600 605	

cag ctg ctg gtt cca tat cta cga tcc aat ctt aca gga ttt aag caa	1993
Gln Leu Leu Val Pro Tyr Leu Arg Ser Asn Leu Thr Gly Phe Lys Gln	
610 615 620	
ctt gaa ata ctt aac ttc aga aac ggg agt gtg att gtg aat agc aaa	2041
Leu Glu Ile Leu Asn Phe Arg Asn Gly Ser Val Ile Val Asn Ser Lys	
625 630 635	
atg aag ttt gct aag tct gtg cgg tat aac ctc acc aag gct gtg cac	2089
Met Lys Phe Ala Lys Ser Val Pro Tyr Asn Leu Thr Lys Ala Val His	
640 645 650	
ggg gtc ttg gag gat ttt cgt tct gct gca gcc caa caa ctc cat ctg	2137
Gly Val Leu Glu Asp Phe Arg Ser Ala Ala Ala Gln Gln Leu His Leu	
655 660 665 670	
gaa ata gac agc tac tct ctc aac att gaa cca gct gat caa gca gat	2185
Glu Ile Asp Ser Tyr Ser Leu Asn Ile Glu Pro Ala Asp Gln Ala Asp	
675 680 685	
ccc tgc aag ttc ctg gcc tgc ggc gaa ttt gcc caa tgt gta aag aac	2233
Pro Cys Lys Phe Leu Ala Cys Gly Glu Phe Ala Gln Cys Val Lys Asn	
690 695 700	
gaa cgg act gag gaa gcg gag tgt cgc tgc aaa cca gga tat gac agc	2281
Glu Arg Thr Glu Glu Ala Glu Cys Arg Cys Lys Pro Gly Tyr Asp Ser	
705 710 715	
cag ggg agc ctg gac ggt ctg gaa cca ggc ctc tgt ggc ctg gca caa	2329
Gln Gly Ser Leu Asp Gly Leu Glu Pro Gly Leu Cys Gly Leu Ala Gln	
720 725 730	
agg aat gcg agg tcc tcc agg gaa agg gag ctc cat gcg gtt cca gat	2377
Arg Asn Ala Arg Ser Ser Arg Glu Arg Glu Leu His Ala Val Pro Asp	
735 740 745 750	
cac tct gaa aat caa gca tac aaa act agt gtt aaa agt tcc aaa atc	2425
His Ser Glu Asn Gln Ala Tyr Lys Thr Ser Val Lys Ser Ser Lys Ile	
755 760 765	
aac aaa ata aca agg taatcagtaa aagaaattct gaattactga ccgtagaata	2480
Asn Lys Ile Thr Arg	
770	
tgaagaattt aaccatcaag attgggaagg aaattaaaaa ctgaaaaatgt acaattatca	2540
cttaggctat ctcaagagag atgatttgcc ttctcaagga aaatggagac aggcatattc	2600
atgggtcatc aaaatccaga catacagtca acactgagaa tcagcacaca ccatatttca	2660
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aatgatcat aagccagggt tgettccacc ttccctgaaa attttactca cagatcattt	2840
gcaacaagca tagcttactt attgtttagg gactgaacaa tttattggga agcaaactct	2900
ttatatgcta gaaagtacat ttaaaagatg actacttacg caggggagatg cagggtctctc	2960
taaacgcatg aatgtatgta gtgtgtaggc actgtagtga gtgtatatat getccacact	3020

acgtctgata aacacaaacc tcagtattca gttattaggc acactagttt tatacgcaac 3080  
 tactgcttac atagtagact gttttgttgc caataatctt tgaattgttc tttaaaagaa 3140  
 actgagggttc agatacacat accatggaaa aatcttactt ttcttgttac tacacaaagc 3200  
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 <213> Homo sapiens  
 <223> Human IPM 150 isoform A variant cDNA sequence

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 20 25 30  
 Thr Lys Asp Ile Asp Asn Pro Pro Arg Asn Glu Thr Thr Glu Ser Thr  
 35 40 45  
 Glu Lys Met Tyr Lys Met Ser Thr Met Arg Arg Ile Phe Asp Leu Ala  
 50 55 60  
 Lys His Arg Thr Lys Arg Ser Ala Phe Phe Pro Thr Gly Val Lys Val  
 65 70 75 80  
 Cys Pro Gln Glu Ser Met Lys Gln Ile Leu Asp Ser Leu Gln Ala Tyr  
 85 90 95  
 Tyr Arg Leu Arg Val Cys Gln Glu Ala Val Trp Glu Ala Tyr Arg Ile  
 100 105 110  
 Phe Leu Asp Arg Ile Pro Asp Thr Gly Glu Tyr Gln Asp Trp Val Ser  
 115 120 125  
 Ile Cys Gln Gln Glu Thr Phe Cys Leu Phe Asp Ile Gly Lys Asn Phe  
 130 135 140  
 Ser Asn Ser Gln Glu His Leu Asp Leu Leu Gln Gln Arg Ile Lys Gln  
 145 150 155 160  
 Arg Ser Phe Pro Asp Arg Lys Asp Glu Ile Ser Ala Glu Lys Thr Leu  
 165 170 175  
 Gly Glu Pro Gly Glu Thr Ile Val Ile Ser Thr Asp Val Ala Asn Val  
 180 185 190  
 Ser Leu Gly Pro Phe Pro Leu Thr Pro Asp Asp Thr Leu Leu Asn Glu  
 195 200 205  
 Ile Leu Asp Asn Thr Leu Asn Asp Thr Lys Met Pro Thr Thr Glu Arg  
 210 215 220

Glu Thr Glu Phe Ala Val Leu Glu Glu Gln Arg Val Glu Leu Ser Val  
 225 230 235 240  
 Ser Leu Val Asn Gln Lys Phe Lys Ala Glu Leu Ala Asp Ser Gln Ser  
 245 250 255  
 Pro Tyr Tyr Gln Glu Leu Ala Gly Lys Ser Gln Leu Gln Met Gln Lys  
 260 265 270  
 Ile Phe Lys Lys Leu Pro Gly Phe Lys Lys Ile His Val Leu Gly Phe  
 275 280 285  
 Arg Pro Lys Lys Glu Lys Asp Gly Ser Ser Ser Thr Glu Met Gln Leu  
 290 295 300  
 Thr Ala Ile Phe Lys Arg His Ser Ala Glu Ala Lys Ser Pro Ala Ser  
 305 310 315 320  
 Asp Leu Leu Ser Phe Asp Ser Asn Lys Ile Glu Ser Glu Glu Val Tyr  
 325 330 335  
 His Gly Thr Met Glu Glu Asp Lys Gln Pro Glu Ile Tyr Leu Thr Ala  
 340 345 350  
 Thr Asp Leu Lys Arg Leu Ile Ser Lys Ala Leu Glu Glu Glu Gln Ser  
 355 360 365  
 Leu Asp Val Gly Thr Ile Gln Phe Thr Asp Glu Ile Ala Gly Ser Leu  
 370 375 380  
 Pro Ala Phe Gly Pro Asp Thr Gln Ser Glu Leu Pro Thr Ser Phe Ala  
 385 390 395 400  
 Val Ile Thr Glu Asp Ala Thr Leu Ser Pro Glu Leu Pro Pro Val Glu  
 405 410 415  
 Pro Gln Leu Glu Thr Val Asp Gly Ala Glu His Gly Leu Pro Asp Thr  
 420 425 430  
 Ser Trp Ser Pro Pro Ala Met Ala Ser Thr Ser Leu Ser Glu Ala Pro  
 435 440 445  
 Pro Phe Phe Met Ala Ser Ser Ile Phe Ser Leu Thr Asp Gln Gly Thr  
 450 455 460  
 Thr Asp Thr Met Ala Thr Asp Gln Thr Met Leu Val Pro Gly Leu Thr  
 465 470 475 480  
 Ile Pro Thr Ser Asp Tyr Ser Ala Ile Ser Gln Leu Ala Leu Gly Ile  
 485 490 495  
 Ser His Pro Pro Ala Ser Ser Asp Asp Ser Arg Ser Ser Ala Gly Gly  
 500 505 510  
 Glu Asp Met Val Arg His Leu Asp Glu Met Asp Leu Ser Asp Thr Pro  
 515 520 525  
 Ala Pro Ser Glu Val Pro Glu Leu Ser Glu Tyr Val Ser Val Pro Asp  
 530 535 540



His Phe Leu Glu Asp Thr Thr Pro Val Ser Ala Leu Gln Tyr Ile Thr  
 545 550 555 560  
 Thr Ser Ser Met Thr Ile Ala Pro Lys Gly Arg Glu Leu Val Val Phe  
 565 570 575  
 Phe Ser Leu Arg Val Ala Asn Met Ala Phe Ser Asn Asp Leu Phe Asn  
 580 585 590  
 Lys Ser Ser Leu Glu Tyr Arg Ala Leu Glu Gln Gln Phe Thr Gln Leu  
 595 600 605  
 Leu Val Pro Tyr Leu Arg Ser Asn Leu Thr Gly Phe Lys Gln Leu Glu  
 610 615 620  
 Ile Leu Asn Phe Arg Asn Gly Ser Val Ile Val Asn Ser Lys Met Lys  
 625 630 635 640  
 Phe Ala Lys Ser Val Pro Tyr Asn Leu Thr Lys Ala Val His Gly Val  
 645 650 655  
 Leu Glu Asp Phe Arg Ser Ala Ala Ala Gln Gln Leu His Leu Glu Ile  
 660 665 670  
 Asp Ser Tyr Ser Leu Asn Ile Glu Pro Ala Asp Gln Ala Asp Pro Cys  
 675 680 685  
 Lys Phe Leu Ala Cys Gly Glu Phe Ala Gln Cys Val Lys Asn Glu Arg  
 690 695 700  
 Thr Glu Glu Ala Glu Cys Arg Cys Lys Pro Gly Tyr Asp Ser Gln Gly  
 705 710 715 720  
 Ser Leu Asp Gly Leu Glu Pro Gly Leu Cys Gly Leu Ala Gln Arg Asn  
 725 730 735  
 Ala Arg Ser Ser Arg Glu Arg Glu Leu His Ala Val Pro Asp His Ser  
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 Ile Thr Arg  
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<210> 29

<211> 20

<212> PRT

<213> Rattus sp.

<220>

<223> Rat IPM 200 N-terminal amino acid sequence

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Ala Glu Ala Val  
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<210> 30  
<211> 10  
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<223> Xaa is any amino acid.

<400> 30  
Xaa Val Leu Phe Pro Asn Gly Val Lys Ile  
1 5 10

<210> 31  
<211> 20  
<212> PRT  
<213> Pig species

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1 5 10 15

Lys Gln Ile Leu  
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<210> 32  
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<212> PRT  
<213> Artificial Sequence

<220>  
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Gly Arg Gly Asp Ser Pro  
1 5

<210> 33  
<211> 6  
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<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
RGD-containing peptide

<400> 33  
Gly Arg Gly Asp Thr Pro  
1 5

<210> 34  
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<223> Xaa is d-Arginine

<400> 34  
Gly Xaa Gly Asp Ser Pro  
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<210> 35  
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<212> PRT  
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<220>  
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peptide

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<223> MeGly

<400> 35  
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<210> 36  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: RGD-containing  
peptide

<400> 36  
Gly Arg Gly Asp Ser Pro Ala Ser Ser Lys  
1 5 10

<210> 37  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Inhibitor

<220>  
<221> MOD\_RES  
<222> (2)

<223> Xaa is pencillamine

<400> 37

Gly Xaa Gly Arg Gly Asp Ser Pro Cys Ala  
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